

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2001, 12:06:43 ; Search time 11.18 Seconds

(Without alignments)
962.095 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641

Sequence: 1 MATCIDTCRTGNTQDDSRF.....IPCLTMDQSTYLTEMSPDYVI 314

Scoring table: BLOSUM62

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match	Length	ID	Description
1	648.5	39.5	273	1	CYSE_ECOLI	P05796 escherichia
2	648.5	39.5	273	1	CYSE_SALTY	P29647 salmonella
3	624.5	38.1	267	1	CYSE_HAEIN	P43886 haemophilus
4	573.5	34.9	274	1	CYSE_BUCAL	P57162 buchnera ap
5	549.5	33.5	261	1	CYSE_BUCAP	P32003 synchococc
6	430.5	26.2	244	1	CYSE_SYNP7	O06002 synchococc
7	424	25.8	217	1	CYSE_BACSU	O06750 bacillus su
8	420.5	25.6	249	1	CYSE_SYNY3	P74089 staphylocyst
9	399	24.3	216	1	CYSE_STAXY	P77985 staphylococ
10	369.5	22.5	269	1	NIFP_AZOC	P23145 azotobacter
11	365	22.2	171	1	CYSE_HELPY	P71405 helicobacte
12	359	21.9	171	1	CYSE_HELPY	O92K14 helicobacte
13	287	17.5	319	1	SRPH_SYNP7	O59667 synchococc
14	217	13.2	162	1	WCAH_ECOLI	F77558 escherichia
15	164.5	10.0	190	1	MODL_RHILV	O08632 rhizobium 1
16	164.5	10.0	214	1	YA64_METUA	O58464 methanococc
17	160	9.8	203	1	YJHA_ECOLI	P07664 escherichia
18	156.5	9.5	196	1	YJHA_YEAST	P40892 saccharomyc
19	153.5	9.4	207	1	YA39_SCHPO	O09707 schizosach
20	150	9.1	183	1	MODL_RHIME	P28266 rickettsia
21	146.5	8.9	346	1	LPXD_RICPR	O92ed3 rickettsia
22	136.5	8.3	184	1	MAA_BACSU	P37515 bacillus su
23	133.5	8.1	345	1	LPXD_RICRI	P32202 rickettsia
24	129.5	7.9	182	1	MAA_ECOLI	O66662 aquifex aco
25	127.5	7.8	261	1	LPXA_AQUAE	P31852 pseudomonas
26	127.5	7.8	276	1	TABB_PESZ	P39856 staphylococ
27	126.5	7.7	172	1	THGA_LACLA	P52984 lactococcus
28	120.5	7.3	207	1	THGA_LACLA	O57752 methanococ
29	117.5	7.3	159	1	WCAF_METUA	P71240 escherichia
30	117.5	7.2	182	1	WCAF_ECOLI	P72215 proteus mir
31	115.5	7.0	267	1	LPXA_PROMI	P43887 haemophilus
32	115	7.0	262	1	LPXA_HAEIN	P32201 yersinia en
33	114.5	7.0	262	1	LPXA_YEREN	

ALIGNMENTS

RESULT 1
CYSE_ECOLI
ID CYSE_ECOLI STANDARD: PRT: 273 AA.
AC P05796:
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
GN CYSE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88009872; PubMed=3309158;
RA Denk D., Boeck A.;
RT "L-cysteine biosynthesis in Escherichia coli: nucleotide sequence and
RT expression of the serine acetyltransferase (cysE) gene from the wild-
RT type and a cysteine-excreting mutant.";
RL J. Gen. Microbiol. 133:515-525(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=90211342; PubMed=2108679;
RA Tel H., Murata K., Kimura A.;
RT "Structure and expression of cysX, the second gene in the Escherichia
RT coli K-12 cys locus.";
RL Biochem. Biophys. Res. Commun. 167:948-955(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=91099514; PubMed=2125278;
RA Migley D.B., Derrick J.P., Shaw W.V.;
RT "The serine acetyltransferase from Escherichia coli. Over-expression,
RT purification and preliminary crystallographic analysis.";
RL FEBS Lett. 277:267-271(1990).
RN [5]
RP SUBUNIT.
RX MEDLINE=20085066; PubMed=10617639;
RA Hindson V.J., Moody P.C., Rowe A.J., Shaw W.V.;
RT "Serine acetyltransferase from Escherichia coli is a dimer of
RT trimers.";
RL J. Biol. Chem. 275:461-466(2000).
CC -I- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE -> COA + O-ACETYL-L-
CC SERINE.
CC -I- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
CC -I- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -I- SUBUNIT: HOMOHETEROMER. DIMER OF A HOMOTRIMER.

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedlorn E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT Influenzae Rd";
 RL Science 269:496-512(1995).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LEPA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC -----
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 CC -----
 CC EMBL: U32743; AAC22265.1; -
 CC DR TIGR: H10606; -
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
 KW Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
 SQ SEQUENCE 267 AA; 29166 MW; 93428DE9D504DBP4 CRC64;

Query Match 38.1%; Score 624.5; DB 1; Length 267;
 Best Local Similarity 48.4%; Pred. No. 2.4e-42;
 Matches 125; Conservative 54; Mismatches 70; Indels 9; Gaps 2;

QY 47 DWIKMLEAKSDVKOEPLISNYIASITSHRSLSALAHILSVKLSNLPNTLFELEI 106
 DB 4 DWQHIROKELAEDEPMASFHSTILKHQWLGALSTLANKLANPIMPISIRETI 63
 QY 107 ISVLESPPEIESTKODLAVKERDPAISYVHCFLEFGFLACQAHRAHILMKONKRI 166
 DB 64 EEAQVSQPSITIDCAACDIOAVRHDPAVELMSPLLYLNGFHAIGSYRTHILYMNKRKS 123
 QY 167 VALLIQNRSESAVDIHGAKIGKGLLDHATGVYIGETAVGVNVSILHGVTIGTGK 226
 DB 124 LALYLNQISVAVDVIDHPAKIGHGIMFDHATGIYGVETIENDVSILQVTLTGATGK 183
 QY 227 QSGDRHPKIDGVYLIGAGSCILGNTITGEGAKISGSVYVAVDPARTTAVGNPARLIGK 286
 DB 184 ESDGRHPKREGSMIGAGKILGNIIEVGKAKIGANSVYLVNPEYATAGVAPARTV--- 240
 QY 287 ENPRKHDKI--PCLTMDQ 302
 DB 241 ----SODKAKAPAFDMNQ 254

RESULT 4
 CYSE_BUCAL STANDARD: PRT; 274 AA.
 AC P57162;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE OR BU054.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OC symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OK NCBI_TaxID=118099;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOKYO 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS";
 RT Nature 407:81-86(2000).
 RL Nature 407:81-86(2000).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LEPA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AP001118; BAB1277.1; -
 CC DR PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
 KW Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
 SQ SEQUENCE 274 AA; 30165 MW; 553D252F1048B6B1 CRC64;

Query Match 34.9%; Score 573.5; DB 1; Length 274;
 Best Local Similarity 48.9%; Pred. No. 2.6e-38;
 Matches 116; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

QY 48 VWIKMLEAKSDVKOEPLISNYIASITSHRSLSALAHILSVKLSNLPNTLFELEI 107
 DB 9 IWNKILYVVSFLKKEPLISDFYOSILQHSFTSSLSYILNKLSTSMISEKKIQGIFD 68
 QY 108 ISVLESPPEIESTKODLAVKERDPAISYVHCFLEFGFLACQAHRAHILMKONKRI 167
 DB 69 DYVLDNRSLTNFYVDIYAVKAVRDPADVDTPLLYLKHFALEAYRISHYLMWGKSL 128
 QY 168 ALLIQNRSESAVDIHGAKIGKGLLDHATGVYIGETAVGVNVSILHGVTIGTGKQ 227
 DB 129 SLYLSRISSESVDIHRAAFIGSGVMDHATGIVGCVTIENDVSILHSVTIGTGKGN 188
 QY 228 -SGDHPKIDGVYLIGAGSCILGNTITGEGAKISGSVYVAVDPARTTAVGNPARLI 283
 DB 189 FSQNHPTIRRGVYIGAGAKILGNIIEVGSAKIGAGSIVLKNPVSVDYVGVPAKIV 245

RESULT 5
 CYSE_BUCAP STANDARD: PRT; 261 AA.
 AC P32003;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OK NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93012960; PubMed=1398077;
 RA Lai C.-Y., Baumann P.;
 RT "Sequence analysis of a DNA fragment from Buchnera aphidicola (an
 RT endosymbiont of aphids) containing genes homologous to dnaG, rpoD,
 RT cyse, and secB";
 RL Gene 119:113-118(1992).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.

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CC EMBL: L14580; AAA21797.1; -
 CC EMBL: D26185; BAA05327.1; -
 CC EMBL: Z99104; CAB11869.1; -
 CC PIR: B53402; B53402.
 CC HSSP: P01246; 1B5T.
 CC Subtilist: B010155; CYSE.
 CC InterPro: IPR001451; -
 CC Pfam: PF00132; hexaped; 2.
 CC PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
 CC Transferrase: Acyltransferase; Cysteine biosynthesis; Repeat.
 CC KW TRANSFERRASE 217 AA; 24143 MW; 14EFA32FA1086D9D CRC64;
 CC SEQUENCE

Query Match 25.8%; Score 424; DB 1; Length 217;
 Best Local Similarity 47.2%; Pred. No. 1.2e-26;
 Matches 91; Conservative 33; Mismatches 63; Indels 6; Gaps 4;

QY 121 KODLIAVERDPACISYVHCFLEKFGFLACQAHRIATTLMKONRKIVALLIONRVSSEF-179
 Db 7 KEDIDYFDQDPARSRFEVILYSGLHAIWARIHALYKRRFYIARLI-SQVSRFFT 65
 QY 180 AVDIHPGAKIGKGLLDHATGVIGETAVVGDVNSILHGVTLGSTGKSGDRHPIKIGDV 239
 Db 66 GIEIHPGATIGREFIDHGMGVIGETCEIGNNVTVQVTLGSGTGEKKRRPTIKDDA 125
 QY 240 LIGAGSCLILNTTIGEGAKIGSGSVVYKVDVPARTAVGNPARLI--GKKNPR--KHDKI 295
 Db 126 LIATGAVVGLISTYVGESEKIGAGSVVLHDVDFSTVVGIGRVVNGKKVRDLNMDL 185
 QY 296 PCLTMDQSYLTYE 308
 Db 186 PDPVADRFKSLDEQ 198

RESULT 8
 CYSE_SYNY3 STANDARD; PRT; 249 AA.
 ID CYSE_SYNY3
 AC P74089; 055209;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAR).
 GN CYSE OR SLR1348.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sakamoto T., Wada H., Nishida I., Ohta H., Murata N.;
 RT "Sequence analysis of a DNA fragment from Synechocystis PCC6803
 RT containing genes homologous to cyst (serine acetyltransferase) and pg1
 RT (glucose-6-phosphate isomerase).";
 RL Plant Mol. Biol. 29:187-187(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97061201; PubMed=8905231;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirotsawa M., Sugitani M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-116(1996).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).

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CC EMBL: D13777; BAA02919.1; -
 CC EMBL: D90912; BAA18167.1; -
 CC InterPro: IPR001451; -
 CC Pfam: PF00132; hexaped; 3.
 CC PROSITE: PS00101; HEXAPEP-TRANSFERASES; 1.
 CC Transferrase: Acyltransferase; Cysteine biosynthesis; Repeat.
 CC KW TRANSFERRASE 80 80 I->S (IN REF. 1).
 CC CONFLICT 80
 CC SEQUENCE 249 AA; 27336 MW; ED5EC58D559DCFB CRC64;

Query Match 25.6%; Score 420.5; DB 1; Length 249;
 Best Local Similarity 44.6%; Pred. No. 2.8e-26;
 Matches 82; Conservative 35; Mismatches 64; Indels 3; Gaps 1;

QY 116 ITESTKODLIAVERDPACISYVHCFLEKFGFLACQAHRIATTLMKONRKIVALLIONRV 175
 Db 1 MNLSLIADRIITFERDPARKNLEVFCEYGLQALLHFRFSRLTGLLPPFRRLMSHA 60
 QY 176 SESFAVDIHPGAKIGKGLLDHATGVIGETAVVGDVNSILHGVTLGSTGKSGDRHPIK 235
 Db 61 REFTGEIHPGAKIGKGLLDHATGVIGETAVVGDVNSILHGVTLGSTGKSGDRHPIK 120
 QY 236 GDCVILGAGSCLILNTTIGEGAKIGSGSVVYKVDVPARTAVGNPARLI--GKKNPRKH 292
 Db 121 GENVVGAGAKVLGNALIGDNVRIGAGSVLHDVDFSTVVGIGRVVNGKKVRDLNMDL 180
 QY 293 DKIP 296
 Db 181 GKIP 184

RESULT 9
 CYSE_STAXY STANDARD; PRT; 216 AA.
 ID CYSE_STAXY
 AC P77985; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAR).
 GN CYSE.
 OS Staphylococcus xylosum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 OX NCBI_TaxID=1288;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=DSM 20267 / C2A.
 RA MEDLINE=97237691; PubMed=9084146;
 RA Fiegler H., Brueckner R.;
 RT "Identification of the serine acetyltransferase gene of Staphylococcus
 RT xylosum.";
 RL FEMS Microbiol. Lett. 148:181-187(1997).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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EMBL: Y07614; CAA68887.1; -

DR InterPro: IPR001451; -

DR Pfam: PF00132; hexapep. 2.

DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; FALSE_NEG.

KW Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.

SEQUENCE 216 AA; 24000 MW; 728FE804A0D7282C CRC64;

Query Match 24.3%; Score 399; DB 1; Length 216;
Best Local Similarity 40.6%; Pred. No. 1,1e-24;
Matches 88; Conservative 41; Mismatches 68; Indels 20; Gaps 5;

QY 115 EIIESTKODLIVAKERDPACISVHCFLEKGFACQAHRIAHLMKONRKIVALLIONR 174
DB 3 KLLKRIKODVNVVFEQDPAARTTLEVTISYAGVHAWSHLHAEHYKKKYYVLARLI-SQ 61
QY 175 VSESF-ANDIHGAKIGKILDHATGVVIGETAVGVGNVSLHGVTLGGTGKOSGRHP 233
DB 62 VYRFETGIEIHGAOIGRLFLDHGMGVVIGETCRIGDNVITYGVTLGGTGKGRKHP 121
QY 234 KIGDDVLIGAGSCILGNTITIGEGAKIGSGVYVVKDVPARTAVGNPARIIGKRNPRK- 291
DB 122 DIGDNLVLNAGKVLGNTITINANNVIGANSVYLVNSPYSYVIGIPGHIV--KQDGRNIG 179
QY 292 ---HDKIPCLMDQTSYLT-----WSDYVI 314
DB 180 KTFEDHRLPDPIYEQLEKOLEKTRNGEIODDYII 216

RESULT 10
NIFP_AZOOH STANDARD; PRT; 269 AA.
AC P23145;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROBABLE SERINE ACETYLTTRANSFERASE (EC 2.3.1.30) (SAT).
GN NIFP.
OS Azotobacter chroococcum mcd 1.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX Azotobacter.
RN NCB1_Taxid=355;
[1]
SEQUENCE FROM N.A.
RA MEDLINE=91358323; PubMed=1885524;
RA Evans D.J., Jones R., Woodley P.R., Milborn J.R., Robson R.L.;
RT "Nucleotide sequence and genetic analysis of the Azotobacter
chroococcum nifuswzm gene cluster, including a new gene (nifp) which
encodes a serine acetyltransferase.";
RL J. Bacteriol. 173:5457-5469(1991).
CC -1- FUNCTION: PROBABLE SERINE ACETYLTTRANSFERASE REQUIRED FOR
OPTIMIZING THE EXPRESSION OF NITROGENASE ACTIVITY. NIFP MAY BE
REQUIRED TO BOOST RATES OF SYNTHESIS OR INTRACELLULAR
CONCENTRATIONS OF CYSTEINE OR METHIONINE.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
SERINE.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
ACETYLTTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC
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DR PIR: D43706; D43706.
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 2.
DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Nitrogen fixation; Transferase; Acyltransferase; Repeat;
KW Cysteine biosynthesis.
SEQUENCE 269 AA; 28578 MW; E0BBCC98266FDBB CRC64;

Query Match 22.5%; Score 369.5; DB 1; Length 269;
Best Local Similarity 42.6%; Pred. No. 3.2e-22;
Matches 83; Conservative 28; Mismatches 63; Indels 21; Gaps 4;

QY 116 IIEESTKODLIVAKERDPACISVHCFLEKGFACQAHRIAHLMKONRKIVALLIONR 169
DB 3 LIAWRKRDICVFERDPAARTTLEVTITPGVNAIMLYKLAHLMRPNLPPRAVVRAR 62
QY 170 LIONRSESEFANDIHGAKIGKILDHATGVVIGETAVGVGNVSLHGVTLGGTGKOSG 229
DB 63 LVSN-----VDIHGAVIGARFFIDHGACVYIGETAGIRDVTLHYGVTLGGTGANG 115
QY 230 DRHFKIGDVLIGAGSCILGNTITIGEGAKIGSGVYVVKDVPARTAVGNPARI--GG 285
DB 116 KRHPTLGDVVLVGAAGAKILPITITIGANARVANSVYVDVPECTVVGIPKVKLRAG 175
QY 286 KENP---RKHKRIP 296
DB 176 QLNRYGIDLHHLIP 190

RESULT 11
CYSE_HELPY STANDARD; PRT; 171 AA.
ID CYSE_HELPY
AC P71405;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE ACETYLTTRANSFERASE (EC 2.3.1.30) (SAT).
GN CYSE OR HP1210.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX Helicobacter.
RN NCB1_Taxid=210;
[1]
SEQUENCE FROM N.A.
RA STRAIN=ATCC 49503 / 60190;
RA Peek R.M., Thompson S.A., Atherton J.C., Blaser M.J., Miller G.G.;
RT "Expression of a novel ulcer-associated gene, *icea*, by *H. pylori*
following contact with gastric epithelium.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[2]

SEQUENCE FROM N.A.
RA STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kellavag A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.W., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen *Helicobacter*
RT *pylori*.";
RL Nature 388:539-547(1997).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC
CC EMBL: M60090; AAA22162.1; -

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DR EMBL; U43917; AAB07027.1; -
DR EMBL; AE000626; AAD08254.1; -
DR TIGR; HP1210; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; 1.
KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
FT VARIANT 5 5 K -> F (IN STRAIN 60190).
FT VARIANT 110 110 S -> T (IN STRAIN 60190).
FT VARIANT 162 162 S -> T (IN STRAIN 60190).
SQ SEQUENCE 171 AA; 18342 MW; 28646D539C2250C3 CRC64;

Query Match 22.2%; Score 365; DB 1; Length 171;
Best Local Similarity 45.2%; Pred. No. 4.1e-22;
Matches 71; Conservative 31; Mismatches 55; Indels 0; Gaps 0;

QY 127 VKERDPCISYVHCFLGKFLACQAHRIHTLMKONKRIVALIIONRSESFAVDIHFG 186
DB 11 VLQEDPARKKWEVLLIPGIIHALCYRLAHAKRRFYFARLSQLARITTEIHPG 70
QY 187 AKIGKGLIDHATGVIGTAVVGDVNSILHGYTLGCTGKSGDRHPRKIGDGLIGAGSC 246
DB 71 AKIGRGLFDHGMGVIGETTEIGDDVTIYHGYTLGCTGKSGDRHPRKIGDGLIGAGSC 130
QY 247 ILGNITIGEGAKIGSGSVYKVDVPTTAVGNPARI 283
DB 131 VLGAICVDVYKIGANAVVLSDLTGSTAVGAKAKTI 167

RESULT 12
CISE_HELPJ STANDARD; PRT; 171 AA.
AC 092K14;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE SERINE ACETYLTANSFERASE (EC 2.3.1.30) (SAT).
GN CYSE OR JHP1133.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan A., Guild B.C., deJonge B.L., Carmel G.,
RA Tummiano P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Voyis G.F.,
RA Trust T.J.;
RT Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
CC ACETYLTANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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DR EMBL; AE001541; AAD06715.1; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 4.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; 1.
KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
SQ SEQUENCE 171 AA; 18354 MW; 2872B7539C3AC14A CRC64;

Query Match 21.9%; Score 359; DB 1; Length 171;
Best Local Similarity 44.6%; Pred. No. 1.2e-21;
Matches 70; Conservative 31; Mismatches 56; Indels 0; Gaps 0;

QY 127 VKERDPCISYVHCFLGKFLACQAHRIHTLMKONKRIVALIIONRSESFAVDIHFG 186
DB 11 VLQEDPARKKWEVLLIPGIIHALCYRLAHAKRRFYFARLSQLARITTEIHPG 70
QY 187 AKIGKGLIDHATGVIGTAVVGDVNSILHGYTLGCTGKSGDRHPRKIGDGLIGAGSC 246
DB 71 AKIGRGLFDHGMGVIGETTEIGDDVTIYHGYTLGCTGKSGDRHPRKIGDGLIGAGSC 130
QY 247 ILGNITIGEGAKIGSGSVYKVDVPTTAVGNPARI 283
DB 131 VLGAICVDVYKIGANAVVLSDLTGSTAVGAKAKTI 167

RESULT 13
SRPH_SYN7 STANDARD; PRT; 319 AA.
AC 059967;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SERINE ACETYLTANSFERASE, PLASMID (EC 2.3.1.30) (SAT).
GN SRPH.
OS Synecoccus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecoccus.
OC Plasmid pANL.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95327059; PubMed=7603442;
RA Nicholson M.L., Gaasenbeek M., Landenbach D.E.;
RT "Two enzymes together capable of cysteine biosynthesis are encoded on
RT a cyanobacterial plasmid.";
RL Mol. Gen. Genet. 247:623-632(1995).
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
CC SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
CC ACETYLTANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC or send an email to license@isb-sib.ch).

DR EMBL; U23436; AAA86726.1; -
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep. 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; FALSE_NEG.
KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat; Plasmid.
SQ SEQUENCE 319 AA; 34570 MW; 00BB74D8AAB1E70 CRC64;

Query Match 17.5%; Score 287; DB 1; Length 319;

Best local Similarity 30.9%; Pred. No. 1,36-15;
Matches 88; Conservative 32; Mismatches 101; Indels 64; Gaps 8)

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QY      47 DVMIKMLEAKSDVKEPILSNVYASTSHRSLSALAHLSV-----KLS----- 93
Db      19 DSIIVALSQASDTPPLPHHLLSDQFY-PLPSRESLQILLHGRSVLPFRHGFDEPELSEVT 77
QY      94 -----NLNL-----PSMT-----PFELFISVLSPE 115
Db      78 HYFICGLTKTLLMLEQIRREMLQHTYQGIPRETPAVLSQHSSELQAFQAPEIKR 137
QY      116 IESTKODLLIAVERDPACISYVHCFGLKFGFLACQAHIAHTMTKONRKIVALLIONRV 175
Db      138 LIDS-----DVNAALALGPAAQSISEILFCYCPGTTATTFHRLAHRLYOLDPLARITAEVS 194
QY      176 SESAVNDIHGKATIGSILLDHNTAGVGVGETVAVSDANYSILHGYTLG-----TGK-- 226
Db      195 HSETGIDIHGGAIGGSFFIDHGTGTVIGETVVIDRRITQATVILKAKSPRDETCALI 254
QY      227 QSGDRHPKIDGVLVLIAGSCILGNTITGEGAKIGSGSVYKDVPA 271
Db      255 KGARHPVEIDEDVVIYAGATLLGRITVGSGSTIGGNVMLTRSVPA 299

RESULT 14
WCAB_ECOLI      STANDARD;      PRT;      162 AA.
ID WCAB_ECOLI
AC P77558;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 01-OCT-2000 (Rel. 40, last annotation update)
DE PUTATIVE COLANIC ACID BIOSYNTHESIS ACETYLTRANSFERASE WCAB
DE (EC 2.3.1.-).
GN WCAB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RC MEDLINE=96326333; Pubmed=8759852;
RA Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
RT "Organization of the Escherichia coli K-12 gene cluster responsible
RT for production of the extracellular polysaccharide colanic acid.";
RL J. Bacteriol. 178:4885-4893(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MGI655;
RC MEDLINE=97426617; Pubmed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RT Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RC MEDLINE=97251358; Pubmed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Saito N., Sempel G., Seki Y., Sivasubaram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horichi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE
CC COLANIC ACID.
CC - SIMILARITY: BELONGS TO THE CYSE/LCA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC -----
DR EMBL; U08473; AAC77837.1; -.
DR EMBL; AE000295; AAC75119.1; -.
DR EMBL; D90843; BAA15911.1; -.
DR EcoGene; EG13570; wcab.
DR InterPro; IPR001451; -.
DR Pfam; PF00132; hexaped; 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
KW lipidpolysaccharide biosynthesis; transferase; Acyltransferase; Repeat
SQ SEQUENCE 162 AA; 17615 MW; F2462836F3FB3AD CRC64;

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Query Match	13.2%	Score 217;	DB 1;	Length 162;
Best Local Similarity	37.1%;	Pred. No. 1.8e-10;		
Matches	52;	Conservative	24;	Mismatches 54;
			Indels	10;
			Gaps	4;

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QY      152 AHRIAH--TLWKQ----NRKIVALLIONRVSES--FAVDIHPGKAKIGKGLLDHATGV 202
        |:|:| |:|:| | |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db      20 AYRAVAFCSVRKKKNVLNLMAPLVIYRIITECFEGYEIQAAATIGRRETIHGCAVV 79
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QY 203 IGETAVAGDNVSIHLGVTILGGTCKOSGDHRPKIGDGLVGAGSCILGNITTEGAKTGS 262
| : | | : : | | | | : | : | | | : | | : | : |
Db 80 INKNVAGDDFTIRHGVTLIGNRADN-MACPHICSGVELCANVILSGDTILGNNAVTVAG 138

QY	263	SVVVKDVPARTTAVGNPARL	282
		: T	:
Db	139	SVVLDSVPDNALVGEKARY	158

RESULT	15	
NODL_RHLY		
ID	NODL_RHLY	STANDARD;
		PRT; 190 AA

AC P08632;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MODULATION PROTEIN L (EC 2.3.1.-).

GN NODL.
05 Rhizobium leguminosarum (biovar viciae).
06 Plasmid sym pRLJ1.
0C Bacteria; proteobacteria; alpha subdivision; Rhizobiaceae group
0C Rhizobiaceae: Rhizobium.
0X NCBI_TaxID=387;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=248;
RX MEDLINE=88246045; PubMed=2132583;
RA Surin B. P.; Downie J.A.;
RT "Characterization of the Rhicobium leguminosarum genes nodJMN
RL involved in efficient host-specific nodulation."; Mol. Microbiol. 2:173-183(1988).

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92003664; PubMed=2563395;
RA Canter Creemers H.C.J., Spaik H.P., Wijffes A.H.M., Pees E.,
RA Wijkfelman C.A., Okker R.J.H., Lugtenberg B.J.J.;
RT "Additional nodulation genes on the Sym plasmid of *Rhizobium*
RT *leguminosarum* biovar *viciae*.";
RL Plant Mol. Biol. 13:163-174(1989).

RN [3]
 RP SIMILARITY TO OTHER MEMBER OF THE CYSE/LACA/NODL FAMILY.
 RX MEDLINE=90136094; PubMed=2615659;
 RA Downie J.A.;
 RT "The nodL gene from *Rhizobium leguminosarum* is homologous to the
 acetyl transferases encoded by laca and cysE.";


```

RL Mol. Microbiol. 3:1649-1651(1989).
CC -1- FUNCTION: ACETYLTRANSFERASE IMPLICATED IN THE O-ACETYLATION OF
CC NOD FACTORS.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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CC -----
DR EMBL; X17557; CAA35590.1; -
DR EMBL; Y00548; CAA68625.1; -
DR PIR; S01039; S01039.
DR PIR; S07000; S07000.
DR InterPro: IPR001451; -
DR Pfam: PF00132; hexapep; 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
DR Plasmid; Nodulation; Transferase; Acyltransferase; Repeat.
KW SEQUENCE 190 AA; 20105 MW; 2ACA4E82D6EDF48C CRC64;
SQ

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Query Match          10.0%; Score 164.5; DB 1; Length 190;
Best Local Similarity 42.7%; Pred. No. 3.1e-06;
Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3;

QY 193 ILIDHATGVVIGETAVVGNVSIL-----HGVTLGSTGKQSGDRHFKTGDGVILGAGSCI 247
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 89 VILDVA-AVTIGDPTAIGPAVOITYADHHDPEQROAGLQGS-REVSTGRHAWIGGAI 146
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 248 LGNITIGEGAKTIGSGVYKVDYPARTAVGNPRLIGKENPR 290
   | :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 147 LQGVITIGDAVIGAGSVYTRDVPAGSTAMGNPARYKAGRLPK 189
   | :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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